

9066 Book No. PURPOSE

cont'd

9 10 15 10 25 30 35 40 45
ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAA AAA AGG TCT
TAC CCA CCT GUA CCT TCT TAC GTC CAC AGA GCA GGG AGG TTT TTC AGA
M G A G G R M Q V S P P S K K S>
50 55 60 65 70 75 80 85 90 95
GAA ACC GAC AAC ATC AAG CCG GTC GCA CCC TCC GAG ACA CGG CCC TTC ACT
CTT TGG CTG CTG TAG TTC GCG CAT CGG AGG CTC TGT GCG GGG AGG TCA
E T D N I K R V P C E T P P F D>
100 105 110 115 120 125 130 135 140
GTC GGA GAA CTC AAG AAA GCA ATC CCA CGG CAC TGT TTC AAA CGG TCG
CGG CCT CTG GAG TTC TTT CGT TAG GTC GTC GCA AAG TTT GGG AGG
V G E L R K A I P P H C F K R S>
145 150 155 160 165 170 175 180 185 190
ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC AIA GCC TCC
TAG GGA CGG AGA AAG AGG ATG GAG TAG ACC CTG TAG TAG TAT CGG AGG
I P R S F S Y L I W D T I I A S>
195 200 205 210 215 220 225 230 235 240
TGC TTC TAC TAC GTC GCG AGC ACT TAC TTC CCT CTC CTC CCT CAC CGT
AGG AGG AGG ATG CGG CGG TCA ATG AAG GGA GAG GGA GTC CGA
C F Y T V A T T Y F P L L P H S>
245 250 255 260 265 270 275 280 285
CTC TCC TAC TPC GCG TGG CCT CTC TAC TGG GCC CAG GGC TGC
GAG AGG ATG AAG CGG ACC GGA GAG ATG ACC CGG ACC GTC CCG AGC
L S Y F A M P L Y H A C>
290 295 300 305 310 315 A CK 320 325 330 335
CTA ACC GGC GTC TGG GTC ATG AAG GCA CGC GAG TGC CGG CAC CAC CGG TTC
GAT TGG CGG CAG ACC CAG TAT CGG GCG CTC AGC CGG GTG GTC CGG AGG
I K V W H M Y F P L L P H S>
340 345 350 355 360 365 370 375 380
AGC GAC TAC CAG TGG CTG GAC GAC ATC GTC GGC CTC ATC TTC CAC TCC
TGG CTC ATG GTC ACC GAC CGG CTG TGG CAG CGG TAG AAC GAG AGG
D T V G L I F H S>
385 390 395 400 405 410 415 420 425 430
TTC CTC CTC GTC CCT TAC TTC TCC AAG TAC AGT CAT COA CGC CAC
AGG GAG GAG CAG GGA ATG AGG AGG ACC TTC ATG TCA GIA GCT GCG GTG
F L L V P Y F S M K Y S H R R H>
435 440 445 450 455 460 465 470 475 480
CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAA GAG TTT GTC CCC AAG
GTA AGG TTC TGA CGG AGG GAG CTC TCT CTC CCT CAC AAA CAG GGG TIC
H S N T G S I E R D E V F V H R>
485 490 495 500 505 510 515 520 525
AAG AGG TCA GAC ATC AAG TGG TAC GGC AAG TAC CTC AAC AAC CCT TGG
TTC TTC ACT CGG TAG TTC AGC ATG CGG TTC ATG GAG TGG TGG GGA AAC
K X S D I K W Y G K Y L N N P L>
530 535 540 545 550 555 560 565 570 575
GGA CGC ACC CGT ATG TTA AGC GTT CAG TTC ACT CTC GGC TGG CCT TGG
CCT CGG TGG CAC TAC ATC TGG CAA GTC AAC TGA GAG CGG ACC GGA AAC
G R T V H L T V Q F I L C W P L>
580 585 590 595 600 605 610 615 620
TAC TTA GGC TTC AAC GTC TGG GGG AGA CCT TAC GAC GGC GGC TTC GCT
ATG ATC CGG AGG TTG CGG AGC CGG CCT GCA ATG CGT CGG CGG AGG CGA
Y L A F B V S G R P Y D G G F A>

DNAs and deduced
protein sequences

from mutant FAD2

(B) clone

In 129 and

Q508 clones

(E)

GA S was converted

to ATG (K)

This mutation

was found in

Exon one only.

This bat occurs

in both 129 and

Q508 mutant

Line

Again, they

Region 643

confirmed from

REMINIDER

For the His

DATE

ISSUED BY

Ch. [Signature]

DATE

TITLE

cont'd

DATE

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PURPOSE

cont'd

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625 630 635 640 645 650 655 660 665 670
 DGC CAT TTC CAC CGC AAC GCT CGC ATC TAC AAC GAC GAC CGC GAG CGT CTC
 ACG GTC AAC GTC GCG TGC CGA GGG TAG ATG TGC TGC CGC CTC GCA GAG
 C H F R P N A P I Y N D R E R L
 675 680 685 690 695 700 705 710 715 720
 CGG ATA TAC ATC TAC TCC GAC GCT GGC ATC CTC CGC TGC TGC TAC GCT CTC
 GTC TAT ATG ATG AGG CTC CGA CGG TAG GAG CGG CGG AGG ATG CCA GAG
 0 1 Y 1 S D A G I L R V C T G L
 725 730 735 740 745 750 755 760 765 770
 TAC CGC TAC GCT GTC CAA CGA GGA GTT GCC TCG ATG GTC TGC TGC TAC
 ATG GCG ATG CUA CGA CGA GTC CCT CAA CGG AGC TAC CGC AGG AGG ATG
 Y R Y A A V O G A S M V C F Y
 775 780 785 790 795 800 805 810 815 820
 GGA GTT CGG CTC CGC ATT GTC ATT GGG TTC TTA GTT TGC ATC ACT TAC
 CCT CAA CGC GAA GGC TAA CGG TAA CGC AAC AGG ATG CAA AAC TAC TGA ATG
 G V P L L I V N G F L V L I T Y
 825 830 835 840 845 850 855 860 865 870
 TTG CAG CAC AGC GAT CCT TCC CTC CCT CAC TAT GAC TCG TCT GAG TGG
 ATC GTC GTC TGC GAA GGA AGG GAC GGA GTC ATA CTG AGC AGA CTC ACC
 L Q H T H P S L P H Y D S S E P
 865 870 875 880 885 890 895 900 905 910
 GAT TGG TTG AGG GAA GCT TTG GGC AGC GTC GAC AGA GAC TAC CGA ATC
 CTA ACC AAC TCC CCT CGA AAC CGG TGG CAA CTG TCT CTG ATG CCT TAG
 D W L R G A L A I V D R D Y G I
 915 920 925 930 935 940 945 950 955 960
 TTG AAC AGG GTC TGC CAC ATT ATC AGC GAC AGC CGC GTG GGG CAT CAC
 AAC TTG TTC CAG AGG GTG TTA TAG TGC CTG TGC GGG CGC CGA GTG
 L N K V F H N I T D T H V A H X
 965 970 975 980 985 990 995 1000 1005 1010
 CTG TTC TCG ACC ATG CGG CAT TAT CAT CGG ATG GAA GCT AGC AGG
 GGC AAC AGG TGG TAC CGC CGC ATA ATA GTC AAC GTC CGC TGC TCC CGC
 L F S T M P H Y H A M E A T K A
 1010 1015 1020 1025 1030 1035 1040 1045 1050 1055
 ATA AAG CGG ATA CTG CGA GAG TAT TAT CAG TGC CAT CGG AGG CGG CGG
 TAT TGC CGC TAT GTC CCT CTC ATA ATA GTC AAC GTC CGC CGC CGC
 I K P I L G E Y Q L H G T P V
 1060 1065 1070 1075 1080 1085 1090 1095 1100
 GTT AAG CGG ATG CGG AGG GAA CGG AAC GAG TGT ATG TAT CTG GAA CGG
 CGA TTC CGC TAC AGC TCC CTC CGC TCC CTC ACA AAC TAC ATA AAC CGC
 V R A M W R E A K E C I Y V E P
 1105 1110 1115 1120 1125 1130 1135 1140 1145 1150
 GAC AGG CGA GGT GAG AGG AAA GGT GTG TTC TGG TAC AAC ATC AAC TTA
 CTG TCC GTT CGA CGC TTC TTC TAT CGA CAC AAC AGC ATG TGG TTA TGC ATG
 D R Q G E K K G V F W Y N N K L
 1155 1160 1165 1170
 TGA AGC AAA GAA CGA AGC AT
 ACT TCC TTT CTC CGT TGT TA
 S K E B T X

both strands

(see pg 2 134)

from primary rotation

Total 5 segments

129 and 250

cross (each with

one) were

Sequence by

primary DR

(see pg 2 134)

and showed the

same orientation

Thus, it appears

to be true

orientation

This will be

further confirmed

by the RT-PCR

and found to be

and agreed by

DR Price